



Supplementary Figure 1:

The figure shows the comparison between sets of spectra identified by InSpecT+SEQUEST and SEQUEST+X!Tandem-K iProphet combinations at 1% error-rate. 29952 spectra are identified by both combinations. Among the 2927 spectra identified only by the InSpecT+SEQUEST combination, 105 are unique to InSpecT, 1738 are matched to the same peptide below error threshold by the other combination, the remaining 1084 are matched to a different peptide below error threshold by the other combination. Among the 1739 spectra identified only by the SEQUEST+X!Tandem-K combination, 8 are unique to X!Tandem, 934 are matched to the same peptide below error threshold by the other combination, the remaining 797 are matched to a different peptide below error threshold by the other combination.

Supplementary Table 1:

| Search Engine | Approximate* Search Speed in PSMs / Sec |
|---------------|---|
| sequest | 1.4 (semi-tryptic) |
| inspect | 1.0 (semi-tryptic) |
| omssa | 1.7 (semi-tryptic) |
| myrimatch | 1.1 (semi-tryptic) |
| tandem | 3.5 (semi-tryptic) |
| mascot | 5.8 (fully-tryptic) |

*Actual search speed is highly dependent on CPU speed, shared jobs on CPU, number of threads used, search parameters, among other factors. These values were collected on different types of CPUs available on our cluster and therefore may not be directly comparable.